



SEQUENCE LISTING

<110> Palese, Peter
O'Neill, Robert

<120> IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS
THAT INHIBIT INTERACTION OF HOST CELL PROTEINS
AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

<130> 6923-119

<140> 10/724,273

<141> 2003-11-24

<150> 08/444,994

<151> 1995-05-19

<150> 08/246,583

<151> 1994-05-20

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> NPI-1 specific primer

<400> 1

gcaaagcagg agaaaccac

19

<210> 2

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> nested NPI-1 primer

<400> 2

gggtccatct gatagatatg agag

24

<210> 3

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' RACE anchor primer

<220>

<221> modified_base

<222> 36, 37, 41, 42, 46, 47

<223> n = i

<400> 3
 cuacuacuac uagggcacgc gtcgactact acgggnnggg nngggngg 48

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GSP-I primer

<400> 4
 tcctgatgtt gctgtagacg 20

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> GSP-II primer

<400> 5
 gcacgactag tatgatttgc 20

<210> 6
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid #15-22 NS1I-1 protein

<400> 6
 Thr Gly Ala Gly Ala Gly Leu Gly
 1 5

<210> 7
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> amino acid #163-167 NS1I-1 protein

<400> 7
 Tyr Ser Ala Ala Lys
 1 5

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> polylinker sequence

<400> 8
 gactggctgg aattcccat ggcgtcc 27

<210> 9
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polylinker sequence

<400> 9
 Asp Trp Leu Glu Phe Pro Met Ala Ser
 1 5

<210> 10
 <211> 2940
 <212> DNA
 <213> Homo sapiens

<220>
 <223> NPI-1 cDNA

<220>
 <221> CDS
 <222> (47)...(1663)

<400> 10
 ctaacttcag cggtggcacc gggatcggtt gccttgagcc tgaaat atg acc acc 55
 Met Thr Thr
 1

cca gga aaa gag aac ttt cgc ctg aaa agt tac aag aac aaa tct ctg 103
 Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn Lys Ser Leu
 5 10 15

aat ccc gat gag atg cgc agg agg agg gag gaa gaa gga ctg cag tta 151
 Asn Pro Asp Glu Met Arg Arg Arg Arg Glu Glu Glu Gly Leu Gln Leu
 20 25 30 35

cga aag cag aaa aga gaa gag cag tta ttc aag cgg aga aat gtt gct 199
 Arg Lys Gln Lys Arg Glu Glu Gln Leu Phe Lys Arg Arg Asn Val Ala
 40 45 50

aca gca gaa gaa gaa aca gaa gaa gaa gtt atg tca gat gga ggc ttt 247
 Thr Ala Glu Glu Glu Thr Glu Glu Glu Val Met Ser Asp Gly Gly Phe
 55 60 65

cat gag gct cag att agt aac atg gag atg gca cca ggt ggt gtc atc 295
 His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly Gly Val Ile
 70 75 80

act tct gac atg att gag atg ata ttt tcc aaa agc cca gag caa cag 343
 Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro Glu Gln Gln
 85 90 95

ctt tca gca aca cag aaa ttc agg aag ctg ctt tca aaa gaa cct aac 391
 Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys Glu Pro Asn
 100 105 110 115

cct cct att gat gaa gtt atc agc aca cca gga gta gtg gcc agg ttt 439
 Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val Ala Arg Phe
 120 125 130

gtg gag ttc ctc aaa cga aaa gag aat tgt tca ctg cag ttt gaa tca	487
Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln Phe Glu Ser	
135 140 145	
gct tgg gta ctg aca aat att gct tca gga aat tct ctt cag acc cga	535
Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu Gln Thr Arg	
150 155 160	
att gtg att cag gca aga gct gtg ccc atc ttc ata gag ttg ctc agc	583
Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu Leu Leu Ser	
165 170 175	
tca gag ttt gaa gat gtc cag gaa cag gca gtc tgg gct ctt ggc aac	631
Ser Glu Phe Glu Asp Val Gln Glu Gln Ala Val Trp Ala Leu Gly Asn	
180 185 190 195	
att gct gga gat agt acc atg tgc agg gac tat gtc tta gac tgc aat	679
Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu Asp Cys Asn	
200 205 210	
atc ctt ccc cct ctt ttg cag tta ttt tca aag caa aac cgc ctg acc	727
Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn Arg Leu Thr	
215 220 225	
atg acc cgg aat gca gta tgg gct ttg tct aat ctc tgt aga ggg aaa	775
Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys Arg Gly Lys	
230 235 240	
agt cca cct cca gaa ttt gca aag gtt tct cca tgt ctg aat gtg ctt	823
Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu Asn Val Leu	
245 250 255	
tcc tgg ttg ctg ttt gtc agt gac act gat gta ctg gct gat gcc tgc	871
Ser Trp Leu Leu Phe Val Ser Asp Thr Asp Val Leu Ala Asp Ala Cys	
260 265 270 275	
tgg gcc ctc tca tat cta tca gat gga ccc aat gat aaa att caa gcg	919
Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys Ile Gln Ala	
280 285 290	
gtc atc gat gcg gga gta tgt agg aga ctt gtg gaa ctg ctg atg cat	967
Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu Leu Met His	
295 300 305	
aat gat tat aaa gtg gtt tct cct gct ttg cga gct gtg gga aac att	1015
Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val Gly Asn Ile	
310 315 320	
gtc aca ggg gat gat att cag aca cag gta att ctg aat tgc tca gct	1063
Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn Cys Ser Ala	
325 330 335	
ctg cag agt tta ttg cat ttg ctg agt agc cca aag gaa tct atc aaa	1111
Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu Ser Ile Lys	
340 345 350 355	
aag gaa gca tgt tgg acg ata tct aat att aca gct gga aat agg gca	1159
Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly Asn Arg Ala	
360 365 370	

cag atc cag act gtg ata gat gcc aac att ttc cca gcc ctc att agt	1207
Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala Leu Ile Ser	
375 380 385	
att tta caa act gct gaa ttt cgg aca aga aaa gaa gca gct tgg gcc	1255
Ile Leu Gln Thr Ala Glu Phe Arg Thr Arg Lys Glu Ala Ala Trp Ala	
390 395 400	
atc aca aat gca act tct gga gga tca gct gaa cag atc aag tac cta	1303
Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile Lys Tyr Leu	
405 410 415	
gta gaa ctg ggt tgt atc aag ccg ctc tgt gat ctc ctc acg gtc atg	1351
Val Glu Leu Gly Cys Ile Lys Pro Leu Cys Asp Leu Leu Thr Val Met	
420 425 430 435	
gac tct aag att gta cag gtt gcc cta aat ggc ttg gaa aat atc ctg	1399
Asp Ser Lys Ile Val Gln Val Ala Leu Asn Gly Leu Glu Asn Ile Leu	
440 445 450	
agg ctt gga gaa cag gaa gcc aaa agg aac ggc act ggc att aac cct	1447
Arg Leu Gly Glu Gln Glu Ala Lys Arg Asn Gly Thr Gly Ile Asn Pro	
455 460 465	
tac tgt gct ttg att gaa gaa gct tat ggt ctg gat aaa att gag ttc	1495
Tyr Cys Ala Leu Ile Glu Glu Ala Tyr Gly Leu Asp Lys Ile Glu Phe	
470 475 480	
tta cag agt cat gaa aac cag gag atc tac caa aag gcc ttt gat ctt	1543
Leu Gln Ser His Glu Asn Gln Glu Ile Tyr Gln Lys Ala Phe Asp Leu	
485 490 495	
att gag cat tac ttc ggg acc gaa gat gaa gac agc agc att gca ccc	1591
Ile Glu His Tyr Phe Gly Thr Glu Asp Glu Asp Ser Ser Ile Ala Pro	
500 505 510 515	
cag gtt gac ctt aac cag cag cag tac atc ttc caa cag tgt gag gct	1639
Gln Val Asp Leu Asn Gln Gln Gln Tyr Ile Phe Gln Gln Cys Glu Ala	
520 525 530	
cct atg gaa ggt ttc cag ctt tga agcaatactc tgctttcacg tacctgtgct	1693
Pro Met Glu Gly Phe Gln Leu *	
535	
cagaccaggc taccagtcg agtcctcttg tggagcccac agtcctcatg gagctaactt	1753
ctcaaattgtt ttccataata ctgtttgcgc tcattttgctt gccttgcgca cctgctctct	1813
tacacacatc tggaaaacct ccggtctctt gtggtgggat acccttctaa taaaagggtta	1873
accagaacgg ccactctctt ttacggaaa aatccctagg ctttgagat ccgcacttac	1933
attagagtta tgggaatata cacatattaa tgtggctccc ttttcttgt gggggaataa	1993
aagaggactc ctctcattc cctttaacat ggggggaaaaa actgacatta aaagatgaga	2053
ctaaatcttt atcttgaatt ttacacaact acttacgaca agggagatgt ttagacctgt	2113
tggtatactt cagagtactt ttcatgagtt cttccacagt gaacccttgg attacctggg	2173
ggctttttct agccagattg cattaatcct tactgagatt ggatggtttt ctttctctta	2233
ttggcgccat tcttcagata ttaaagttaa accatccact ccctcacctt cagccttcag	2293
tgaatgtgct ttctagttgt caggaatgct gaagaattaa cactttgact cctaaatgtg	2353
atactgggtg gtaagagcag ggcacattta atttgttcgc ttttgcttct ctttgggtctg	2413
ggcacattta atttgttcgc ttttgcttct ctttgggtctt ttcgaatact tagtaatcga	2473
aaaccatatt ctgtaattta ataaaaaaa ctaaggacga aaaaaccctt ccaattttcc	2533
caaatgcaat cagtgttaact aggggctgtg tttctgcatt aaaataaatg tttcaggctt	2593
tgtggctctg atcaaggtcc tcattaaaaa attggagttc accctaggct tttccctctt	2653
gtgactggca gataacacat acttttgaaa gtaacttttg gatttttttt cttaggtgca	2713

```

gctcgattct aatcttttca tgctgcacac gattccttta atcgatagca tccttatctg 2773
aaagaaataa ccattcttctc aacatgacct gcttaaccca aataagaaca gtgatcttat 2833
aacctcattg tttcctaatac tattttatatt catctcctgc tagtactgtg ccgcttcccc 2893
ctccccccac acaaaataaa aacagtatct cgcttctggc tcatttt 2940

```

```

<210> 11
<211> 538
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> deduced protein sequence from NPI-1 cDNA

```

```

<400> 11
Met Thr Thr Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn
 1          5          10          15
Lys Ser Leu Asn Pro Asp Glu Met Arg Arg Arg Arg Glu Glu Glu Gly
          20          25          30
Leu Gln Leu Arg Lys Gln Lys Arg Glu Glu Gln Leu Phe Lys Arg Arg
          35          40          45
Asn Val Ala Thr Ala Glu Glu Glu Thr Glu Glu Glu Val Met Ser Asp
          50          55          60
Gly Gly Phe His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly
65          70          75          80
Gly Val Ile Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro
          85          90          95
Glu Gln Gln Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys
          100          105          110
Glu Pro Asn Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val
          115          120          125
Ala Arg Phe Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln
          130          135          140
Phe Glu Ser Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu
145          150          155          160
Gln Thr Arg Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu
          165          170          175
Leu Leu Ser Ser Glu Phe Glu Asp Val Gln Glu Gln Ala Val Trp Ala
          180          185          190
Leu Gly Asn Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu
          195          200          205
Asp Cys Asn Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn
          210          215          220
Arg Leu Thr Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys
225          230          235          240
Arg Gly Lys Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu
          245          250          255
Asn Val Leu Ser Trp Leu Leu Phe Val Ser Asp Thr Asp Val Leu Ala
          260          265          270
Asp Ala Cys Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys
          275          280          285
Ile Gln Ala Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu
          290          295          300
Leu Met His Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val
305          310          315          320
Gly Asn Ile Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn
          325          330          335
Cys Ser Ala Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu
          340          345          350
Ser Ile Lys Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly
          355          360          365
Asn Arg Ala Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala

```

370	375	380
Leu Ile Ser Ile Leu	Gln Thr Ala Glu Phe	Arg Thr Arg Lys Glu Ala
385	390	395
Ala Trp Ala Ile Thr	Asn Ala Thr Ser Gly Gly	Ser Ala Glu Gln Ile
	405	410
Lys Tyr Leu Val Glu	Leu Gly Cys Ile Lys	Pro Leu Cys Asp Leu Leu
	420	425
Thr Val Met Asp Ser	Lys Ile Val Gln Val Ala	Leu Asn Gly Leu Glu
	435	440
Asn Ile Leu Arg Leu	Gly Glu Gln Glu Ala Lys	Arg Asn Gly Thr Gly
	450	455
Ile Asn Pro Tyr Cys	Ala Leu Ile Glu Glu Ala	Tyr Gly Leu Asp Lys
465	470	475
Ile Glu Phe Leu Gln	Ser His Glu Asn Gln Glu	Ile Tyr Gln Lys Ala
	485	490
Phe Asp Leu Ile Glu	His Tyr Phe Gly Thr Glu	Asp Glu Asp Ser Ser
	500	505
Ile Ala Pro Gln Val	Asp Leu Asn Gln Gln Gln	Tyr Ile Phe Gln Gln
	515	520
Cys Glu Ala Pro Met	Glu Gly Phe Gln Leu	
530	535	

<210> 12
 <211> 542
 <212> PRT
 <213> Homo sapiens

<220>
 <223> SRP1 protein

<400> 12
Met Asp Asn Gly Thr Asp Ser Ser Thr Ser Lys Phe Val Pro Glu Tyr
1 5 10 15
Arg Arg Thr Asn Phe Lys Asn Lys Gly Arg Phe Ser Ala Asp Glu Leu
20 25 30
Arg Arg Arg Arg Asp Thr Gln Gln Val Glu Leu Arg Lys Ala Lys Arg
35 40 45
Asp Glu Ala Leu Ala Lys Arg Arg Asn Phe Ile Pro Pro Thr Asp Gly
50 55 60
Ala Asp Ser Asp Glu Glu Asp Glu Ser Ser Val Ser Ala Asp Gln Gln
65 70 75 80
Phe Tyr Ser Gln Leu Gln Gln Glu Leu Pro Gln Met Thr Gln Gln Leu
85 90 95
Asn Ser Asp Asp Met Gln Glu Gln Leu Ser Ala Thr Val Lys Phe Arg
100 105 110
Gln Ile Leu Ser Arg Glu His Arg Pro Pro Ile Asp Val Val Ile Gln
115 120 125
Ala Gly Val Val Pro Arg Leu Val Glu Phe Met Arg Glu Asn Gln Pro
130 135 140
Glu Met Leu Gln Leu Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser
145 150 155 160
Gly Thr Ser Ala Gln Thr Lys Val Val Val Asp Ala Asp Ala Val Pro
165 170 175
Leu Phe Ile Gln Leu Leu Tyr Thr Gly Ser Val Glu Val Lys Glu Gln
180 185 190
Ala Ile Trp Ala Leu Gly Asn Val Ala Gly Asp Ser Thr Asp Tyr Arg
195 200 205
Asp Tyr Val Leu Gln Cys Asn Ala Met Glu Pro Ile Leu Gly Leu Phe
210 215 220
Asn Ser Asn Lys Pro Ser Leu Ile Arg Thr Ala Thr Trp Thr Leu Ser

225					230					235				240
Asn	Leu	Cys	Arg	Gly	Lys	Lys	Pro	Gln	Pro	Asp	Trp	Ser	Val	Val
				245					250					255
Gln	Ala	Leu	Pro	Thr	Leu	Ala	Lys	Leu	Ile	Tyr	Ser	Met	Asp	Thr
			260					265					270	
Thr	Leu	Val	Asp	Ala	Cys	Trp	Ala	Ile	Ser	Tyr	Leu	Ser	Asp	Gly
		275					280					285		Pro
Gln	Glu	Ala	Ile	Gln	Ala	Val	Ile	Asp	Val	Arg	Ile	Pro	Lys	Arg
	290					295					300			
Val	Glu	Leu	Leu	Ser	His	Glu	Ser	Thr	Leu	Val	Gln	Thr	Pro	Ala
	305				310					315				320
Arg	Ala	Val	Gly	Asn	Ile	Val	Thr	Gly	Asn	Asp	Leu	Gln	Thr	Gln
				325					330					335
Val	Ile	Asn	Ala	Gly	Val	Leu	Pro	Ala	Leu	Arg	Leu	Leu	Leu	Ser
			340					345					350	Ser
Pro	Lys	Glu	Asn	Ile	Lys	Lys	Glu	Ala	Cys	Trp	Thr	Ile	Ser	Asn
		355					360					365		Ile
Thr	Ala	Gly	Asn	Thr	Glu	Gln	Ile	Gln	Ala	Val	Ile	Asp	Ala	Asn
	370				375						380			Leu
Ile	Pro	Pro	Leu	Val	Lys	Leu	Leu	Glu	Val	Ala	Glu	Tyr	Lys	Thr
	385				390					395				400
Lys	Glu	Ala	Cys	Trp	Ala	Ile	Ser	Asn	Ala	Ser	Ser	Gly	Gly	Leu
			405					410						Gln
Arg	Pro	Asp	Ile	Ile	Arg	Tyr	Leu	Val	Ser	Gln	Gly	Cys	Ile	Lys
			420				425						430	Pro
Leu	Cys	Asp	Leu	Leu	Glu	Ile	Ala	Asp	Asn	Arg	Ile	Ile	Glu	Val
		435				440						445		Thr
Leu	Asp	Ala	Leu	Glu	Asn	Ile	Leu	Lys	Met	Gly	Glu	Ala	Asp	Lys
	450				455					460				Glu
Ala	Arg	Gly	Leu	Asn	Ile	Asn	Glu	Asn	Ala	Asp	Phe	Ile	Glu	Lys
	465				470				475					Ala
Gly	Gly	Met	Glu	Lys	Ile	Phe	Asn	Cys	Gln	Gln	Asn	Glu	Asn	Asp
			485					490					495	Lys
Ile	Tyr	Glu	Lys	Ala	Tyr	Lys	Ile	Ile	Glu	Thr	Tyr	Phe	Gly	Glu
		500					505					510		Glu
Glu	Asp	Ala	Val	Asp	Glu	Thr	Met	Ala	Pro	Gln	Asn	Ala	Gly	Asn
	515					520					525			Thr
Phe	Gly	Phe	Gly	Ser	Asn	Val	Asn	Gln	Gln	Phe	Asn	Phe	Asn	
	530				535					540				

<210> 13
 <211> 170
 <212> DNA
 <213> Homo sapiens

<220>
 <223> partial nucleotide sequence of NPI-2

<400> 13
 ggaggcaccg aagggcagcg ccgagtcgga gggggcgaag attgacgccg gtaagaacga 60
 ggaggatgaa ggccattcaa actcctcccc acgacactct gaagcagcga cggcacagcg 120
 ggaagaatgg aaaatgttta taggagcct tagctgggac actacaaaga 170

<210> 14
 <211> 1827
 <212> DNA
 <213> Homo sapiens

<220>
 <223> partial nucleotide sequence of NPI-3

<220>

<221> CDS

<222> (1)...(1362)

<400> 14

gag gtc aat gtg gag ctg agg aaa gct aag aag gat gac cag atg ctg	48
Glu Val Asn Val Glu Leu Arg Lys Ala Lys Lys Asp Asp Gln Met Leu	
1 5 10 15	
aag agg aga aat gta agc tca ttt cct gat gat gct act tct ccg ctg	96
Lys Arg Arg Asn Val Ser Ser Phe Pro Asp Asp Ala Thr Ser Pro Leu	
20 25 30	
cag gaa aac cgc aac aac cag ggc act gta aat tgg tct gtt gat gac	144
Gln Glu Asn Arg Asn Asn Gln Gly Thr Val Asn Trp Ser Val Asp Asp	
35 40 45	
att gtc aaa ggc ata aat agc agc aat gtg gaa aat cag ctc caa gct	192
Ile Val Lys Gly Ile Asn Ser Ser Asn Val Glu Asn Gln Leu Gln Ala	
50 55 60	
act caa gct gcc agg aaa cta ctt tcc aga gaa aaa cag ccc ccc ata	240
Thr Gln Ala Ala Arg Lys Leu Leu Ser Arg Glu Lys Gln Pro Pro Ile	
65 70 75 80	
gac aac ata atc cgg gct ggt ttg att ccg aaa ttt gtg tcc ttc ttg	288
Asp Asn Ile Ile Arg Ala Gly Leu Ile Pro Lys Phe Val Ser Phe Leu	
85 90 95	
ggc aga act gat tgt agt ccc att cag ttt gaa tct gct tgg gca ctc	336
Gly Arg Thr Asp Cys Ser Pro Ile Gln Phe Glu Ser Ala Trp Ala Leu	
100 105 110	
act aac att gct tct ggg aca tca gaa caa acc aag gct gtg gta gat	384
Thr Asn Ile Ala Ser Gly Thr Ser Glu Gln Thr Lys Ala Val Val Asp	
115 120 125	
gga ggt gcc atc cca gca ttc att tct ctg ttg gca tct ccc cat gct	432
Gly Gly Ala Ile Pro Ala Phe Ile Ser Leu Leu Ala Ser Pro His Ala	
130 135 140	
cac atc agt gaa caa gct gtc tgg gct cta gga aac att gca ggt gat	480
His Ile Ser Glu Gln Ala Val Trp Ala Leu Gly Asn Ile Ala Gly Asp	
145 150 155 160	
ggc tca gtg ttc cga gac ttg gtt att aag tac ggt gca gtt gac cca	528
Gly Ser Val Phe Arg Asp Leu Val Ile Lys Tyr Gly Ala Val Asp Pro	
165 170 175	
ctg ttg gct ctc ctt gca gtt cct gat atg tca tct tta gca tgt ggc	576
Leu Leu Ala Leu Leu Ala Val Pro Asp Met Ser Ser Leu Ala Cys Gly	
180 185 190	
tac tta cgt aat ctt acc tgg aca ctt tct aat ctt tgc cgc aac aag	624
Tyr Leu Arg Asn Leu Thr Trp Thr Leu Ser Asn Leu Cys Arg Asn Lys	
195 200 205	
aat cct gca ccc ccg ata gat gct gtt gag cag att ctt cct acc tta	672
Asn Pro Ala Pro Pro Ile Asp Ala Val Glu Gln Ile Leu Pro Thr Leu	
210 215 220	

gtt cgg ctc ctg cat cat gat gat cca gaa gtg tta gca gat acc tgc	720
Val Arg Leu Leu His His Asp Asp Pro Glu Val Leu Ala Asp Thr Cys	
225 230 235 240	
tgg gct att tcc tac ctt act gat ggt cca aat gaa cga att ggc atg	768
Trp Ala Ile Ser Tyr Leu Thr Asp Gly Pro Asn Glu Arg Ile Gly Met	
245 250 255	
gtg gtg aaa aca gga gtt gtg ccc caa ctt gtg aag ctt cta gga gct	816
Val Val Lys Thr Gly Val Val Pro Gln Leu Val Lys Leu Leu Gly Ala	
260 265 270	
tct gaa ttg cca att gtg act cct gcc cta aga gcc ata ggg aat att	864
Ser Glu Leu Pro Ile Val Thr Pro Ala Leu Arg Ala Ile Gly Asn Ile	
275 280 285	
gtc act ggt aca gat gaa cag act cag gtt gtg att gat gca gga gca	912
Val Thr Gly Thr Asp Glu Gln Thr Gln Val Val Ile Asp Ala Gly Ala	
290 295 300	
ctc gcc gtc ttt ccc agc ctg ctc acc aac ccc aaa act aac att cag	960
Leu Ala Val Phe Pro Ser Leu Leu Thr Asn Pro Lys Thr Asn Ile Gln	
305 310 315 320	
aag gaa gct acg tgg aca atg tca aac atc aca gcc ggc cgc cag gac	1008
Lys Glu Ala Thr Trp Thr Met Ser Asn Ile Thr Ala Gly Arg Gln Asp	
325 330 335	
cag ata cag caa gtt gtg aat cat gga tta gtc cca ttc ctt gtc agt	1056
Gln Ile Gln Gln Val Val Asn His Gly Leu Val Pro Phe Leu Val Ser	
340 345 350	
gtt ctc tct aag gca gat ttt aag aca caa aag gaa gct gtg tgg gcc	1104
Val Leu Ser Lys Ala Asp Phe Lys Thr Gln Lys Glu Ala Val Trp Ala	
355 360 365	
gtg acc aac tat acc agt ggt gga aca gtt gaa cag att gtg tac ctt	1152
Val Thr Asn Tyr Thr Ser Gly Gly Thr Val Glu Gln Ile Val Tyr Leu	
370 375 380	
gtt cac tgt ggc ata ata gaa ccg ttg atg aac ctc tta act gca aaa	1200
Val His Cys Gly Ile Ile Glu Pro Leu Met Asn Leu Leu Thr Ala Lys	
385 390 395 400	
gat acc aag att att ctg gtt atc ctg gat gcc att tca aat atc ttt	1248
Asp Thr Lys Ile Ile Leu Val Ile Leu Asp Ala Ile Ser Asn Ile Phe	
405 410 415	
cag gct gct gag aaa cta ggt gaa act agc tgc ccg tct tca cag att	1296
Gln Ala Ala Glu Lys Leu Gly Glu Thr Ser Cys Pro Ser Ser Gln Ile	
420 425 430	
caa gaa caa ggg aaa aga cag tac aga aat gag gcg tcc gag gcg tcg	1344
Gln Glu Gln Gly Lys Arg Gln Tyr Arg Asn Glu Ala Ser Glu Ala Ser	
435 440 445	
cag aat aga gaa act tag tataatgatt gaagaatgtg gaggcttaga	1392
Gln Asn Arg Glu Thr *	
450	

```

caaaattgaa gctctacaaa accatgaaaa tgagtctgtg tataaggcctt cgtaaagcctt 1452
aattgagaag tatttctctg tagaggaaga ggaagatcaa aacgttgtac cagaaactac 1512
ctctgaaggc tacactttcc aagttcagga tggggctcct gggaccttta acttttagat 1572
catgtagctg agacataaat ttgttggtga ctacgtttgg tattttgtct tattgtttct 1632
ctactaagaa ctctttctta aatgtggttt gttactgtag cactttttac actgaaacta 1692
tacttgaaca gttccaactg tacatacata ctgtatgaag cttgtcctct gactagggtt 1752
ctaatttcta tgtggaattt cctatcttgc agcatcctgt aaataaacat tcaagtccac 1812
ccttttcttg acttc 1827

```

<210> 15

<211> 453

<212> PRT

<213> Homo sapiens

<220>

<223> partial nucleotide sequence of NPI-3

<400> 15

```

Glu Val Asn Val Glu Leu Arg Lys Ala Lys Lys Asp Asp Gln Met Leu
1      5      10      15
Lys Arg Arg Asn Val Ser Ser Phe Pro Asp Asp Ala Thr Ser Pro Leu
20     25     30
Gln Glu Asn Arg Asn Asn Gln Gly Thr Val Asn Trp Ser Val Asp Asp
35     40     45
Ile Val Lys Gly Ile Asn Ser Ser Asn Val Glu Asn Gln Leu Gln Ala
50     55     60
Thr Gln Ala Ala Arg Lys Leu Leu Ser Arg Glu Lys Gln Pro Pro Ile
65     70     75     80
Asp Asn Ile Ile Arg Ala Gly Leu Ile Pro Lys Phe Val Ser Phe Leu
85     90     95
Gly Arg Thr Asp Cys Ser Pro Ile Gln Phe Glu Ser Ala Trp Ala Leu
100    105    110
Thr Asn Ile Ala Ser Gly Thr Ser Glu Gln Thr Lys Ala Val Val Asp
115    120    125
Gly Gly Ala Ile Pro Ala Phe Ile Ser Leu Leu Ala Ser Pro His Ala
130    135    140
His Ile Ser Glu Gln Ala Val Trp Ala Leu Gly Asn Ile Ala Gly Asp
145    150    155    160
Gly Ser Val Phe Arg Asp Leu Val Ile Lys Tyr Gly Ala Val Asp Pro
165    170    175
Leu Leu Ala Leu Leu Ala Val Pro Asp Met Ser Ser Leu Ala Cys Gly
180    185    190
Tyr Leu Arg Asn Leu Thr Trp Thr Leu Ser Asn Leu Cys Arg Asn Lys
195    200    205
Asn Pro Ala Pro Pro Ile Asp Ala Val Glu Gln Ile Leu Pro Thr Leu
210    215    220
Val Arg Leu Leu His His Asp Asp Pro Glu Val Leu Ala Asp Thr Cys
225    230    235    240
Trp Ala Ile Ser Tyr Leu Thr Asp Gly Pro Asn Glu Arg Ile Gly Met
245    250    255
Val Val Lys Thr Gly Val Val Pro Gln Leu Val Lys Leu Leu Gly Ala
260    265    270
Ser Glu Leu Pro Ile Val Thr Pro Ala Leu Arg Ala Ile Gly Asn Ile
275    280    285
Val Thr Gly Thr Asp Glu Gln Thr Gln Val Val Ile Asp Ala Gly Ala
290    295    300
Leu Ala Val Phe Pro Ser Leu Leu Thr Asn Pro Lys Thr Asn Ile Gln
305    310    315    320
Lys Glu Ala Thr Trp Thr Met Ser Asn Ile Thr Ala Gly Arg Gln Asp
325    330    335
Gln Ile Gln Gln Val Val Asn His Gly Leu Val Pro Phe Leu Val Ser

```


aacgggggggt ca

372

<210> 19

<211> 2675

<212> DNA

<213> Homo sapiens

<220>

<223> nucleotide sequence of NS1I-1

<220>

<221> CDS

<222> (104)...(2311)

<400> 19

tctgaccctc gtcccgcccc cgccattcgc cgctcctcc tgtcccgag tcggcggtcca 60
gcggtctctgc ttgttcgtgt gtgtgtcgtt gcaggcctta ttc atg ggc tca ccg 115
Met Gly Ser Pro
1

ctg agg ttc gac ggg cgg gtg gta ctg gtc acc ggc gcg ggg gca gga 163
Leu Arg Phe Asp Gly Arg Val Val Leu Val Thr Gly Ala Gly Ala Gly
5 10 15 20

ttg ggc cga gcc tat gcc ctg gct ttt gca gaa aga gga gcg tta gtt 211
Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg Gly Ala Leu Val
25 30 35

gtt gtg aat gat ttg gga ggg gac ttc aaa gga gtt ggt aaa ggc tcc 259
Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val Gly Lys Gly Ser
40 45 50

tta gct gat aag gtt gtt gaa gaa ata aga agg aga ggt gga aaa gca 307
Leu Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg Gly Gly Lys Ala
55 60 65

gtg gcc aac tat gat tca gtg gaa gaa gga gag aag gtt gtg aag aca 355
Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys Val Val Lys Thr
70 75 80

gcc ctg gat gct ttt gga aga ata gat gtt gtg gtc aac aat gct gga 403
Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val Asn Asn Ala Gly
85 90 95 100

att ctg agg gat cat tcc ttt gct agg ata agt gat gaa gac tgg gat 451
Ile Leu Arg Asp His Ser Phe Ala Arg Ile Ser Asp Glu Asp Trp Asp
105 110 115

ata atc cac aga gtt cat ttg cgg ggt tca ttc caa gtg aca cgg gca 499
Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln Val Thr Arg Ala
120 125 130

gca tgg gaa cac atg aag aaa cag aag tat gga agg att att atg act 547
Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg Ile Ile Met Thr
135 140 145

tca tca gct tca gga ata tat ggc aac ttt ggc cag gcc aat tat agt 595
Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln Ala Asn Tyr Ser
150 155 160

gct gca aag ttg ggt ctt ctg ggc ctt gca aat tct ctt gca att gaa 643

Ala	Ala	Lys	Leu	Gly	Leu	Leu	Gly	Leu	Ala	Asn	Ser	Leu	Ala	Ile	Glu	
165					170					175					180	
ggc	agg	aaa	agc	aac	att	cat	tgt	aac	acc	att	gct	cct	aat	gcg	gga	691
Gly	Arg	Lys	Ser	Asn	Ile	His	Cys	Asn	Thr	Ile	Ala	Pro	Asn	Ala	Gly	
				185					190					195		
tca	cgg	atg	act	cag	aca	gtt	atg	cct	gaa	gat	ctt	gtg	gaa	gcc	ttg	739
Ser	Arg	Met	Thr	Gln	Thr	Val	Met	Pro	Glu	Asp	Leu	Val	Glu	Ala	Leu	
			200					205					210			
aag	cca	gag	tat	gtg	gca	cct	ctt	gtc	ctt	tgg	ctt	tgt	cac	gag	agt	787
Lys	Pro	Glu	Tyr	Val	Ala	Pro	Leu	Val	Leu	Trp	Leu	Cys	His	Glu	Ser	
		215					220					225				
tgt	gag	gag	aat	ggc	ggc	ttg	ttt	gag	gtt	ggc	gca	gga	tgg	att	gga	835
Cys	Glu	Glu	Asn	Gly	Gly	Leu	Phe	Glu	Val	Gly	Ala	Gly	Trp	Ile	Gly	
	230					235					240					
aaa	tta	cgc	tgg	gag	cgg	act	ctt	gga	gct	att	gta	aga	caa	aag	aat	883
Lys	Leu	Arg	Trp	Glu	Arg	Thr	Leu	Gly	Ala	Ile	Val	Arg	Gln	Lys	Asn	
245					250					255					260	
cac	cca	atg	act	cct	gag	gca	gtc	aag	gct	aac	tgg	aag	aag	atc	tgt	931
His	Pro	Met	Thr	Pro	Glu	Ala	Val	Lys	Ala	Asn	Trp	Lys	Lys	Ile	Cys	
				265					270					275		
gac	ttt	gag	aat	gcc	agc	aag	cct	cag	agt	atc	caa	gaa	tca	act	ggc	979
Asp	Phe	Glu	Asn	Ala	Ser	Lys	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Thr	Gly	
			280					285					290			
agt	ata	att	gaa	gtt	ctg	agt	aaa	ata	gat	tca	gaa	gga	gga	gtt	tca	1027
Ser	Ile	Ile	Glu	Val	Leu	Ser	Lys	Ile	Asp	Ser	Glu	Gly	Gly	Val	Ser	
		295					300					305				
gca	aat	cat	act	agt	cgt	gca	acg	tct	aca	gca	aca	tca	gga	ttt	gct	1075
Ala	Asn	His	Thr	Ser	Arg	Ala	Thr	Ser	Thr	Ala	Thr	Ser	Gly	Phe	Ala	
	310					315					320					
gga	gct	att	ggc	cag	aaa	ctc	cct	cca	ttt	tct	tat	gct	tat	acg	gaa	1123
Gly	Ala	Ile	Gly	Gln	Lys	Leu	Pro	Pro	Phe	Ser	Tyr	Ala	Tyr	Thr	Glu	
325				330						335					340	
ctg	gaa	gct	att	atg	tat	gcc	ctt	gga	gtg	gga	gcg	tca	atc	aag	gat	1171
Leu	Glu	Ala	Ile	Met	Tyr	Ala	Leu	Gly	Val	Gly	Ala	Ser	Ile	Lys	Asp	
				345					350					355		
cca	aaa	gat	ttg	aaa	ttt	att	tat	gaa	gga	agt	tct	gat	ttc	tcc	tgt	1219
Pro	Lys	Asp	Leu	Lys	Phe	Ile	Tyr	Glu	Gly	Ser	Ser	Asp	Phe	Ser	Cys	
			360					365					370			
ttg	ccc	acc	ttc	gga	gtt	atc	ata	ggc	cag	aaa	tct	atg	atg	ggc	gga	1267
Leu	Pro	Thr	Phe	Gly	Val	Ile	Ile	Gly	Gln	Lys	Ser	Met	Met	Gly	Gly	
		375					380					385				
gga	tta	gca	gaa	att	cct	gga	ctt	tca	atc	aac	ttt	gca	aag	gtt	ctt	1315
Gly	Leu	Ala	Glu	Ile	Pro	Gly	Leu	Ser	Ile	Asn	Phe	Ala	Lys	Val	Leu	
	390					395					400					
cat	gga	gag	cag	tac	tta	gag	tta	tat	aaa	cca	ctt	ccc	aga	gca	gga	1363
His	Gly	Glu	Gln	Tyr	Leu	Glu	Leu	Tyr	Lys	Pro	Leu	Pro	Arg	Ala	Gly	

405		410		415		420	
aaa tta aaa tgt gaa gca gtt gtt gct gat gtc cta gat aaa gga tcc	1411						
Lys Leu Lys Cys Glu Ala Val Val Ala Asp Val Leu Asp Lys Gly Ser							
		425		430		435	
ggt gta gtg att att atg gat gtc tat tct tat tct gag aag gaa ctt	1459						
Gly Val Val Ile Ile Met Asp Val Tyr Ser Tyr Ser Glu Lys Glu Leu		440		445		450	
ata tgc cac aat cag ttc tct ctc ttt ctt gtt ggc tct gga ggc ttt	1507						
Ile Cys His Asn Gln Phe Ser Leu Phe Leu Val Gly Ser Gly Gly Phe		455		460		465	
ggt gga aaa cgg aca tca gac aaa gtc aag gta gct gta gcc ata cct	1555						
Gly Gly Lys Arg Thr Ser Asp Lys Val Lys Val Ala Val Ala Ile Pro		470		475		480	
aat aga cct cct gat gct gta ctt aca gat acc acc tct ctt aat cag	1603						
Asn Arg Pro Pro Asp Ala Val Leu Thr Asp Thr Thr Ser Leu Asn Gln		485		490		495	500
gct gct ttg tac cgc ctc agt gga gac cgg aat ccc tta cac att gat	1651						
Ala Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp		505		510		515	
cct aac ttt gct agt cta gca ggt ttt gac aag ccc ata tta cat gga	1699						
Pro Asn Phe Ala Ser Leu Ala Gly Phe Asp Lys Pro Ile Leu His Gly		520		525		530	
tta tgt aca ttt gga ttt tct gcc agg cgt gtg tta cag cag ttt gca	1747						
Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val Leu Gln Gln Phe Ala		535		540		545	
gat aat gat gtg tca aga ttc aag gca gtt aag gct cgt ttt gca aaa	1795						
Asp Asn Asp Val Ser Arg Phe Lys Ala Val Lys Ala Arg Phe Ala Lys		550		555		560	
cca gta tat cca gga caa act cta caa act gag atg tgg aag gaa gga	1843						
Pro Val Tyr Pro Gly Gln Thr Leu Gln Thr Glu Met Trp Lys Glu Gly		565		570		575	580
aac aga att cat ttt caa acc aag gtc caa gaa act gga gac att gtc	1891						
Asn Arg Ile His Phe Gln Thr Lys Val Gln Glu Thr Gly Asp Ile Val		585		590		595	
att tca aat gca tat gtg gat ctt gca cca aca tct ggt act tca gct	1939						
Ile Ser Asn Ala Tyr Val Asp Leu Ala Pro Thr Ser Gly Thr Ser Ala		600		605		610	
aag aca ccc tct gag ggc ggg aag ctt cag agt acc ttt gta ttt gag	1987						
Lys Thr Pro Ser Glu Gly Gly Lys Leu Gln Ser Thr Phe Val Phe Glu		615		620		625	
gaa ata gga cgc cgc cta aag gat att ggg cct gag gtg gtg aag aaa	2035						
Glu Ile Gly Arg Arg Leu Lys Asp Ile Gly Pro Glu Val Val Lys Lys		630		635		640	
gta aat gct gta ttt gag tgg cat ata acc aaa ggc gga aat att ggg	2083						
Val Asn Ala Val Phe Glu Trp His Ile Thr Lys Gly Gly Asn Ile Gly		645		650		655	660

gct aag tgg act att gac ctg aaa agt ggt tct gga aaa gtg tac caa	2131
Ala Lys Trp Thr Ile Asp Leu Lys Ser Gly Ser Gly Lys Val Tyr Gln	
665 670 675	
ggc cct gca aaa ggt gct gct gat aca aca atc ata ctt tca gat gaa	2179
Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile Ile Leu Ser Asp Glu	
680 685 690	
gat ttc atg gag gtg gtc ctg ggc aag ctt gac cct cag aag gca ttc	2227
Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp Pro Gln Lys Ala Phe	
695 700 705	
ttt agt ggc agg ctg aag gcc aga ggg aac atc atg ctg agc cag aaa	2275
Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile Met Leu Ser Gln Lys	
710 715 720	
ctt cag atg att ctt aaa gac tac gcc aag ctc tga agggcacact	2321
Leu Gln Met Ile Leu Lys Asp Tyr Ala Lys Leu *	
725 730 735	
acactatttaa taaaaatgga atcattaaat actctcttca cccaaatatg cttgattatt	2381
ctgcaaaaagt gattagaact aagatgcagg ggaaattgct taacattttc agatatcaga	2441
taactgcaga ttttcatttt ctactaattt ttcattgtatc attattttta caaggaacta	2501
tatataagct agcacataat tatccttctg ttcttagatc tgtatcttca taataaaaaa	2561
attttgccca agtcctgttt ccttagaatt tgtgatagca ttgataagtt gaaaggaaaa	2621
ttaaatacaat aaaggccttt gataccttta aaaaaaaaaa aaaaaaaaaa aaaa	2675

<210> 20

<211> 735

<212> PRT

<213> Homo sapiens

<220>

<223> protein sequence of NS1I-1

<400> 20

Met Gly Ser Pro Leu Arg Phe Asp Gly Arg Val Val Leu Val Thr Gly	
1 5 10 15	
Ala Gly Ala Gly Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg	
20 25 30	
Gly Ala Leu Val Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val	
35 40 45	
Gly Lys Gly Ser Leu Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg	
50 55 60	
Gly Gly Lys Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys	
65 70 75 80	
Val Val Lys Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val	
85 90 95	
Asn Asn Ala Gly Ile Leu Arg Asp His Ser Phe Ala Arg Ile Ser Asp	
100 105 110	
Glu Asp Trp Asp Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln	
115 120 125	
Val Thr Arg Ala Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg	
130 135 140	
Ile Ile Met Thr Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln	
145 150 155 160	
Ala Asn Tyr Ser Ala Ala Lys Leu Gly Leu Leu Gly Leu Ala Asn Ser	
165 170 175	
Leu Ala Ile Glu Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile Ala	
180 185 190	

Pro	Asn	Ala	Gly	Ser	Arg	Met	Thr	Gln	Thr	Val	Met	Pro	Glu	Asp	Leu
		195					200					205			
Val	Glu	Ala	Leu	Lys	Pro	Glu	Tyr	Val	Ala	Pro	Leu	Val	Leu	Trp	Leu
	210					215					220				
Cys	His	Glu	Ser	Cys	Glu	Glu	Asn	Gly	Gly	Leu	Phe	Glu	Val	Gly	Ala
225					230					235					240
Gly	Trp	Ile	Gly	Lys	Leu	Arg	Trp	Glu	Arg	Thr	Leu	Gly	Ala	Ile	Val
				245					250					255	
Arg	Gln	Lys	Asn	His	Pro	Met	Thr	Pro	Glu	Ala	Val	Lys	Ala	Asn	Trp
			260					265					270		
Lys	Lys	Ile	Cys	Asp	Phe	Glu	Asn	Ala	Ser	Lys	Pro	Gln	Ser	Ile	Gln
	275						280					285			
Glu	Ser	Thr	Gly	Ser	Ile	Ile	Glu	Val	Leu	Ser	Lys	Ile	Asp	Ser	Glu
	290					295					300				
Gly	Gly	Val	Ser	Ala	Asn	His	Thr	Ser	Arg	Ala	Thr	Ser	Thr	Ala	Thr
305					310					315					320
Ser	Gly	Phe	Ala	Gly	Ala	Ile	Gly	Gln	Lys	Leu	Pro	Pro	Phe	Ser	Tyr
				325					330					335	
Ala	Tyr	Thr	Glu	Leu	Glu	Ala	Ile	Met	Tyr	Ala	Leu	Gly	Val	Gly	Ala
			340					345					350		
Ser	Ile	Lys	Asp	Pro	Lys	Asp	Leu	Lys	Phe	Ile	Tyr	Glu	Gly	Ser	Ser
	355						360					365			
Asp	Phe	Ser	Cys	Leu	Pro	Thr	Phe	Gly	Val	Ile	Ile	Gly	Gln	Lys	Ser
	370					375					380				
Met	Met	Gly	Gly	Gly	Leu	Ala	Glu	Ile	Pro	Gly	Leu	Ser	Ile	Asn	Phe
385					390					395					400
Ala	Lys	Val	Leu	His	Gly	Glu	Gln	Tyr	Leu	Glu	Leu	Tyr	Lys	Pro	Leu
				405					410					415	
Pro	Arg	Ala	Gly	Lys	Leu	Lys	Cys	Glu	Ala	Val	Val	Ala	Asp	Val	Leu
			420					425					430		
Asp	Lys	Gly	Ser	Gly	Val	Val	Ile	Ile	Met	Asp	Val	Tyr	Ser	Tyr	Ser
	435						440					445			
Glu	Lys	Glu	Leu	Ile	Cys	His	Asn	Gln	Phe	Ser	Leu	Phe	Leu	Val	Gly
	450				455						460				
Ser	Gly	Gly	Phe	Gly	Gly	Lys	Arg	Thr	Ser	Asp	Lys	Val	Lys	Val	Ala
465					470					475					480
Val	Ala	Ile	Pro	Asn	Arg	Pro	Pro	Asp	Ala	Val	Leu	Thr	Asp	Thr	Thr
				485					490					495	
Ser	Leu	Asn	Gln	Ala	Ala	Leu	Tyr	Arg	Leu	Ser	Gly	Asp	Arg	Asn	Pro
			500					505					510		
Leu	His	Ile	Asp	Pro	Asn	Phe	Ala	Ser	Leu	Ala	Gly	Phe	Asp	Lys	Pro
	515					520						525			
Ile	Leu	His	Gly	Leu	Cys	Thr	Phe	Gly	Phe	Ser	Ala	Arg	Arg	Val	Leu
	530					535					540				
Gln	Gln	Phe	Ala	Asp	Asn	Asp	Val	Ser	Arg	Phe	Lys	Ala	Val	Lys	Ala
545					550					555					560
Arg	Phe	Ala	Lys	Pro	Val	Tyr	Pro	Gly	Gln	Thr	Leu	Gln	Thr	Glu	Met
				565					570					575	
Trp	Lys	Glu	Gly	Asn	Arg	Ile	His	Phe	Gln	Thr	Lys	Val	Gln	Glu	Thr
			580					585					590		
Gly	Asp	Ile	Val	Ile	Ser	Asn	Ala	Tyr	Val	Asp	Leu	Ala	Pro	Thr	Ser
	595						600					605			
Gly	Thr	Ser	Ala	Lys	Thr	Pro	Ser	Glu	Gly	Gly	Lys	Leu	Gln	Ser	Thr
	610					615					620				
Phe	Val	Phe	Glu	Glu	Ile	Gly	Arg	Arg	Leu	Lys	Asp	Ile	Gly	Pro	Glu
625					630					635					640
Val	Val	Lys	Lys	Val	Asn	Ala	Val	Phe	Glu	Trp	His	Ile	Thr	Lys	Gly
				645					650					655	
Gly	Asn	Ile	Gly	Ala	Lys	Trp	Thr	Ile	Asp	Leu	Lys	Ser	Gly	Ser	Gly
		660						665					670		
Lys	Val	Tyr	Gln	Gly	Pro	Ala	Lys	Gly	Ala	Ala	Asp	Thr	Thr	Ile	Ile

		675					680					685				
Leu	Ser	Asp	Glu	Asp	Phe	Met	Glu	Val	Val	Leu	Gly	Lys	Leu	Asp	Pro	
	690					695					700					
Gln	Lys	Ala	Phe	Phe	Ser	Gly	Arg	Leu	Lys	Ala	Arg	Gly	Asn	Ile	Met	
705					710					715					720	
Leu	Ser	Gln	Lys	Leu	Gln	Met	Ile	Leu	Lys	Asp	Tyr	Ala	Lys	Leu		
				725					730					735		